

What is claim d is:

1. A modeling method for predicting an hepatitis B patient to response to interferon treatment, comprising the steps of:

5 STR genotyping;

associating significant STR markers with response of interferon treatment by Monte-Carlo estimation;

testing alleles on significant STR markers;

transferring significant alleles to genotype information;

10 and

generating an equation based on said genotype information.

2. A method according to claim 1, wherein said STR
15 genotyping comprises the steps of:

amplifying STR marker fragments from genomic DNA; and
detecting and analyzing STR polymorphism.

3. A method according to claim 1, wherein said
20 associating significant STR markers with response of interferon treatment comprises obtaining loci correlated with drug response.

4. A method according to claim 1, wherein said testing
alleles comprises analyzing a contingency table.

5. A method according to claim 1, wherein said transferring significant alleles to genotype information comprises constructing a genotype contingency table.

5 6. A method according to claim 1, wherein said generating an equation comprises transferring said genotype information to a binary dataset.

10 7. A method according to claim 6, wherein said generating an equation is practiced by a logistic regression.

8. A method according to claim 1, wherein said testing alleles comprises an allele frequency difference test.

15 9. A method according to claim 1, wherein said transferring significant alleles to genotype information comprises a genotype frequency difference test.

20 10. A method according to claim 1, further comprising selecting a plurality of STR markers to form a combination for said generating an equation.

25 11. A method according to claim 10, further comprising selecting a second plurality of STR markers to form a second combination for estimating an error rate for said first combination.

12. A method according to claim 10, wherein said plurality of STR markers includes 5 STR markers.

5 13. A model for predicting an hepatitis B patient to response to interferon treatment, comprising:

 a combination composed of a plurality of STR markers
 selected from a STR marker set; and

 an equation derived from said combination by
10 Monte-Carlo estimation for indicating said hepatitis B
 patient as high response rate, ambiguous, or low
 response rate.

 14. A model according to claim 13, wherein said
15 combination includes 5 STR markers.